

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Berlin, Vivian
Chiu, Isabel

(ii) TITLE OF INVENTION:

(iii) NUMBER OF SEQUENCES: 25

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LAHIVE & COCKFIELD
(B) STREET: 60 State Street
(C) CITY: Boston
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02109

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: ASCII (text)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Vincent, Matthew P.
(B) REGISTRATION NUMBER: 36,709
(C) REFERENCE/DOCKET NUMBER: MII-036CP

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 227-7400
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 486 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

5	CTC ACC CGT CAC AAT GCA GCC AAC AAG ATC TTG AAG AAC ATG TGT GAA Leu Thr Arg His Asn Ala Ala Asn Lys Ile Leu Lys Asn Met Cys Glu	48
	1 5 10 15	
10	CAC AGC AAC ACG CTG GTC CAG CAG GCC ATG ATG GTG AGT GAA GAG CTG His Ser Asn Thr Leu Val Gln Gln Ala Met Met Val Ser Glu Glu Leu	96
	20 25 30	
15	ATT CGG GTA GCC ATC CTC TGG CAT GAG ATG TGG CAT GAA GGC CTG GAA Ile Arg Val Ala Ile Leu Trp His Glu Met Trp His Glu Gly Leu Glu	144
	35 40 45	
20	GAG GCA TCT CGC TTG TAC TTT GGG GAG AGG AAC GTG AAA GGC ATG TTT Glu Ala Ser Arg Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly Met Phe	192
	50 55 60	
25	GAG GTG CTG GAG CCC CTG CAT GCT ATG ATG GAA CGG GGT CCC CGG ACT Glu Val Leu Glu Pro Leu His Ala Met Met Glu Arg Gly Pro Arg Thr	240
	65 70 75 80	
30	CTG AAG GAA ACA TCC TTT AAT CAG GCA TAT GGC CGA GAT TTA ATG GAG Leu Lys Glu Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu	288
	85 90 95	
35	GCA CAA GAA TGG TGT CGA AAG TAC ATG AAG TCG GGG AAC GTC AAG GAC Ala Gln Glu Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp	336
	100 105 110	
40	CTC ACG CAA GCC TGG GAC CTC TAC TAT CAC GTG TTC AGA CGG ATC TCA Leu Thr Gln Ala Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser	384
	115 120 125	
45	AAG CAG CTA CCC CAG CTC ACA TCC CTG GAG CTG CAG TAT GTG TCC CCC Lys Gln Leu Pro Gln Leu Thr Ser Leu Glu Leu Gln Tyr Val Ser Pro	432
	130 135 140	
50	AAA CTT CTG ATG TGC CGA GAC CTT GAG TTG GCT GTG CCA GGA ACA TAC Lys Leu Leu Met Cys Arg Asp Leu Glu Leu Ala Val Pro Gly Thr Tyr	480
	145 150 155 160	
55	GAC CCC Asp Pro	486

(2) INFORMATION FOR SEQ ID NO:2:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 162 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

1 Leu Thr Arg His Asn Ala Ala Asn Lys Ile Leu Lys Asn Met Cys Glu
 5 20 25 30
 10 35 40 45
 15 50 55 60
 65 70 75 80
 20 100 105 110
 25 115 120 125
 30 130 135 140
 145 150 155 160
 Asp Pro

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGTTTGGA TTCCTAATAA TGTCTGTACA AGTAGAAACC

40

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

5

GGGTTTCGGG ATCCCGTCAT TCCAGTTTCA CAAC

34

(2) INFORMATION FOR SEQ ID NO:5:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

20

- (A) NAME/KEY: CDS
- (B) LOCATION: 14..325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

25

GGAATTCCTA ATA ATG TCC GTA CAA GTA GAA ACC ATC TCC CCA GGA GAC
Met Ser Val Gln Val Glu Thr Ile Ser Pro Gly Asp
1 5 10

49

30

GGG CGC ACC TTC CCC AAG CGC GGC CAG ACC TGC GTG GTG CAC TAC ACC
Gly Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr
15 20 25

97

35

GGG ATG CTT GAA GAT GGA AAG AAA TTT GAT TCC TCC CGT GAC CGT AAC
Gly Met Leu Glu Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn
30 35 40

145

40

AAG CCC TTT AAG TTT ATG CTA GGC AAG CAG GAG GTG ATC CGA GGC TGG
Lys Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp
45 50 55 60

193

45

GAA GAA GGG GTT GCC CAG ATG AGT GTG GGT CAG CGT GCC AAA CTG ACT
Glu Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr
65 70 75

241

ATA TCT CCA GAT TAT GCC TAT GGT GCC ACT GGG CAC CCA GGC ATC ATC
Ile Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile
80 85 90

289

50

CCA CCA CAT GCC ACT CTC GTC TTC GAT GTG GAG CTT CTAAACTGG
Pro Pro His Ala Thr Leu Val Phe Asp Val Glu Leu
95 100

335

55

AATGACGGGA TCC

348

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

10 Met Ser Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1 5 10 15
Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
20 25 30
15 Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
35 40 45
Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
20 50 55 60
Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65 70 75 80
25 Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
85 90 95
Thr Leu Val Phe Asp Val Glu Leu
100
30

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

40 (ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

45

TCGCCGGAAT TCGGGGGCGG AGGTGGAGGA GTACAAGTAG AAACCATC

48

(2) INFORMATION FOR SEQ ID NO:8:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGGTTTCGGG ATCCCGTCAT TCCAGTTTGA GAAG

34

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGCGGATCCG CGCATTATTA CTTGTTTTGA TTGATTTTTT G

41

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGCGGATCCG CGTAAAAGCA AAGTACTATC AATTGAGCCG

40

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5430 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..5427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTG GAG CAC AGT GGG ATT GGA AGA ATC AAA GAG CAG AGT GCC CGC ATG
Leu Glu His Ser Gly Ile Gly Arg Ile Lys Glu Gln Ser Ala Arg Met

48

	1			5					10					15			
5	CTG	GGG	CAC	CTG	GTC	TCC	AAT	GCC	CCC	CGA	CTC	ATC	CGC	CCC	TAC	ATG	96
	Leu	Gly	His	Leu	Val	Ser	Asn	Ala	Pro	Arg	Leu	Ile	Arg	Pro	Tyr	Met	
				20					25					30			
10	GAG	CCT	ATT	CTG	AAG	GCA	TTA	ATT	TTG	AAA	CTG	AAA	GAT	CCA	GAC	CCT	144
	Glu	Pro	Ile	Leu	Lys	Ala	Leu	Ile	Leu	Lys	Leu	Lys	Asp	Pro	Asp	Pro	
				35					40					45			
15	GAT	CCA	AAC	CCA	GGT	GTG	ATC	AAT	AAT	GTC	CTG	GCA	ACA	ATA	GGA	GAA	192
	Asp	Pro	Asn	Pro	Gly	Val	Ile	Asn	Asn	Val	Leu	Ala	Thr	Ile	Gly	Glu	
				50					55					60			
20	TTG	GCA	CAG	GTT	AGT	GGC	CTG	GAA	ATG	AGG	AAA	TGG	GTT	GAT	GAA	CTT	240
	Leu	Ala	Gln	Val	Ser	Gly	Leu	Glu	Met	Arg	Lys	Trp	Val	Asp	Glu	Leu	
				65			70					75				80	
25	TTT	ATT	ATC	ATC	ATG	GAC	ATG	CTC	CAG	GAT	TCC	TCT	TTG	TTG	GCC	AAA	288
	Phe	Ile	Ile	Ile	Met	Asp	Met	Leu	Gln	Asp	Ser	Ser	Leu	Leu	Ala	Lys	
					85					90					95		
30	AGG	CAG	GTG	GCT	CTG	TGG	ACC	CTG	GGA	CAG	TTG	GTG	GCC	AGC	ACT	GGC	336
	Arg	Gln	Val	Ala	Leu	Trp	Thr	Leu	Gly	Gln	Leu	Val	Ala	Ser	Thr	Gly	
				100					105					110			
35	TAT	GTA	GTA	GAG	CCC	TAC	AGG	AAG	TAC	CCT	ACT	TTG	CTT	GAG	GTG	CTA	384
	Tyr	Val	Val	Glu	Pro	Tyr	Arg	Lys	Tyr	Pro	Thr	Leu	Leu	Glu	Val	Leu	
				115					120					125			
40	CTG	AAT	TTT	CTG	AAG	ACT	GAG	CAG	AAC	CAG	GGT	ACA	CGC	AGA	GAG	GCC	432
	Leu	Asn	Phe	Leu	Lys	Thr	Glu	Gln	Asn	Gln	Gly	Thr	Arg	Arg	Glu	Ala	
				130					135					140			
45	ATC	CGT	GTG	TTA	GGG	CTT	TTA	GGG	GCT	TTG	GAT	CCT	TAC	AAG	CAC	AAA	480
	Ile	Arg	Val	Leu	Gly	Leu	Leu	Gly	Ala	Leu	Asp	Pro	Tyr	Lys	His	Lys	
				145			150					155				160	
50	GTG	AAC	ATT	GGC	ATG	ATA	GAC	CAG	TCC	CGG	GAT	GCC	TCT	GCT	GTC	AGC	528
	Val	Asn	Ile	Gly	Met	Ile	Asp	Gln	Ser	Arg	Asp	Ala	Ser	Ala	Val	Ser	
					165					170					175		
55	CTG	TCA	GAA	TCC	AAG	TCA	AGT	CAG	GAT	TCC	TCT	GAC	TAT	AGC	ACT	AGT	576
	Leu	Ser	Glu	Ser	Lys	Ser	Ser	Gln	Asp	Ser	Ser	Asp	Tyr	Ser	Thr	Ser	
				180					185					190			
60	GAA	ATG	CTG	GTC	AAC	ATG	GGA	AAC	TTG	CCT	CTG	GAT	GAG	TTC	TAC	CCA	624
	Glu	Met	Leu	Val	Asn	Met	Gly	Asn	Leu	Pro	Leu	Asp	Glu	Phe	Tyr	Pro	
				195					200					205			
65	GCT	GTG	TCC	ATG	GTG	GCC	CTG	ATG	CGG	ATC	TTC	CGA	GAC	CAG	TCA	CTC	672
	Ala	Val	Ser	Met	Val	Ala	Leu	Met	Arg	Ile	Phe	Arg	Asp	Gln	Ser	Leu	
				210					215					220			
70	TCT	CAT	CAT	CAC	ACC	ATG	GTT	GTC	CAG	GCC	ATC	ACC	TTC	ATC	TTC	AAG	720
	Ser	His	His	His	Thr	Met	Val	Val	Gln	Ala	Ile	Thr	Phe	Ile	Phe	Lys	
						225			230				235			240	

	TCC	CTG	GGA	CTC	AAA	TGT	GTG	CAG	TTC	CTG	CCC	CAG	GTC	ATG	CCC	ACG	768
	Ser	Leu	Gly	Leu	Lys	Cys	Val	Gln	Phe	Leu	Pro	Gln	Val	Met	Pro	Thr	
					245					250					255		
5	TTC	CTT	AAT	GTC	ATT	CGA	GTC	TGT	GAT	GGG	GCC	ATC	CGG	GAA	TTT	TTG	816
	Phe	Leu	Asn	Val	Ile	Arg	Val	Cys	Asp	Gly	Ala	Ile	Arg	Glu	Phe	Leu	
				260				265					270				
10	TTC	CAG	CAG	CTG	GGA	ATG	TTG	GTG	TCC	TTT	GTG	AAG	AGC	CAC	ATC	AGA	864
	Phe	Gln	Gln	Leu	Gly	Met	Leu	Val	Ser	Phe	Val	Lys	Ser	His	Ile	Arg	
				275				280					285				
15	CCT	TAT	ATG	GAT	GAA	ATA	GTC	ACC	CTC	ATG	AGA	GAA	TTC	TGG	GTC	ATG	912
	Pro	Tyr	Met	Asp	Glu	Ile	Val	Thr	Leu	Met	Arg	Glu	Phe	Trp	Val	Met	
		290					295					300					
20	AAC	ACC	TCA	ATT	CAG	AGC	ACG	ATC	ATT	CTT	CTC	ATT	GAG	CAA	ATT	GTG	960
	Asn	Thr	Ser	Ile	Gln	Ser	Thr	Ile	Ile	Leu	Leu	Ile	Glu	Gln	Ile	Val	
	305					310					315					320	
25	GTA	GCT	CTT	GGG	GGT	GAA	TTT	AAG	CTC	TAC	CTG	CCC	CAG	CTG	ATC	CCA	1008
	Val	Ala	Leu	Gly	Gly	Glu	Phe	Lys	Leu	Tyr	Leu	Pro	Gln	Leu	Ile	Pro	
				325					330						335		
30	CAC	ATG	CTG	CGT	GTC	TTC	ATG	CAT	GAC	AAC	AGC	CCA	GGC	CGC	ATT	GTC	1056
	His	Met	Leu	Arg	Val	Phe	Met	His	Asp	Asn	Ser	Pro	Gly	Arg	Ile	Val	
				340				345						350			
35	TCT	ATC	AAG	TTA	CTG	GCT	GCA	ATC	CAG	CTG	TTT	GGC	GCC	AAC	CTG	GAT	1104
	Ser	Ile	Lys	Leu	Leu	Ala	Ala	Ile	Gln	Leu	Phe	Gly	Ala	Asn	Leu	Asp	
			355					360					365				
40	GAC	TAC	CTG	CAT	TTA	CTG	CTG	CCT	CCT	ATT	GTT	AAG	TTG	TTT	GAT	GCC	1152
	Asp	Tyr	Leu	His	Leu	Leu	Leu	Pro	Pro	Ile	Val	Lys	Leu	Phe	Asp	Ala	
		370					375					380					
45	CCT	GAA	GCT	CCA	CTG	CCA	TCT	CGA	AAG	GCA	GCG	CTA	GAG	ACT	GTG	GAC	1200
	Pro	Glu	Ala	Pro	Leu	Pro	Ser	Arg	Lys	Ala	Ala	Leu	Glu	Thr	Val	Asp	
	385					390					395					400	
50	CGC	CTG	ACG	GAG	TCC	CTG	GAT	TTC	ACT	GAC	TAT	GCC	TCC	CGG	ATC	ATT	1248
	Arg	Leu	Thr	Glu	Ser	Leu	Asp	Phe	Thr	Asp	Tyr	Ala	Ser	Arg	Ile	Ile	
				405					410						415		
55	CAC	CCT	ATT	GTT	CGA	ACA	CTG	GAC	CAG	AGC	CCA	GAA	CTG	CGC	TCC	ACA	1296
	His	Pro	Ile	Val	Arg	Thr	Leu	Asp	Gln	Ser	Pro	Glu	Leu	Arg	Ser	Thr	
				420				425						430			
60	GCC	ATG	GAC	ACG	CTG	TCT	TCA	CTT	GTT	TTT	CAG	CTG	GGG	AAG	AAG	TAC	1344
	Ala	Met	Asp	Thr	Leu	Ser	Ser	Leu	Val	Phe	Gln	Leu	Gly	Lys	Lys	Tyr	
			435					440					445				
65	CAA	ATT	TTC	ATT	CCA	ATG	GTG	AAT	AAA	GTT	CTG	GTG	CGA	CAC	CGA	ATC	1392
	Gln	Ile	Phe	Ile	Pro	Met	Val	Asn	Lys	Val	Leu	Val	Arg	His	Arg	Ile	
		450					455					460					
70	AAT	CAT	CAG	CGC	TAT	GAT	GTG	CTC	ATC	TGC	AGA	ATT	GTC	AAG	GGA	TAC	1440
	Asn	His	Gln	Arg	Tyr	Asp	Val	Leu	Ile	Cys	Arg	Ile	Val	Lys	Gly	Tyr	

	465		470		475		480	
	ACA CTT GCT GAT GAA GAG GAG GAT CCT TTG ATT TAC CAG CAT CGG ATG							1488
5	Thr Leu Ala Asp	Glu Glu Glu Asp	Pro Leu Ile Tyr Gln His Arg Met					
		485		490			495	
	CTT AGG AGT GGC CAA GGG GAT GCA TTG GCT AGT GGA CCA GTG GAA ACA							1536
	Leu Arg Ser Gly Gln Gly Asp Ala Leu Ala Ser Gly Pro Val Glu Thr							
10		500		505			510	
	GGA CCC ATG AAG AAA CTG CAC GTC AGC ACC ATC AAC CTC CAA AAG GCC							1584
	Gly Pro Met Lys Lys Leu His Val Ser Thr Ile Asn Leu Gln Lys Ala							
		515		520			525	
15	TGG GGC GCT GCC AGG AGG GTC TCC AAA GAT GAC TGG CTG GAA TGG CTG							1632
	Trp Gly Ala Ala Arg Arg Val Ser Lys Asp Asp Trp Leu Glu Trp Leu							
		530		535			540	
	AGA CGG CTG AGC CTG GAG CTG CTG AAG GAC TCA TCA TCG CCC TCC CTG							1680
20	Arg Arg Leu Ser Leu Glu Leu Leu Lys Asp Ser Ser Ser Pro Ser Leu							
		545		550			555	560
	CGC TCC TGC TGG GCC CTG GCA CAG GCC TAC AAC CCG ATG GCC AGG GAT							1728
25	Arg Ser Cys Trp Ala Leu Ala Gln Ala Tyr Asn Pro Met Ala Arg Asp							
		565		570			575	
	CTC TTC AAT GCT GCA TTT GTG TCC TGC TGG TCT GAA CTG AAT GAA GAT							1776
	Leu Phe Asn Ala Ala Phe Val Ser Cys Trp Ser Glu Leu Asn Glu Asp							
30		580		585			590	
	CAA CAG GAT GAG CTC ATC AGA AGC ATC GAG TTG GCC CTC ACC TCA CAA							1824
	Gln Gln Asp Glu Leu Ile Arg Ser Ile Glu Leu Ala Leu Thr Ser Gln							
		595		600			605	
35	GAC ATC GCT GAA GTC ACA CAG ACC CTC TTA AAC TTG GCT GAA TTC ATG							1872
	Asp Ile Ala Glu Val Thr Gln Thr Leu Leu Asn Leu Ala Glu Phe Met							
		610		615			620	
	GAA CAC AGT GAC AAG GGC CCC CTG CCA CTG AGA GAT GAC AAT GGC ATT							1920
40	Glu His Ser Asp Lys Gly Pro Leu Pro Leu Arg Asp Asp Asn Gly Ile							
		625		630			635	640
	GTT CTG CTG GGT GAG AGA GCT GCC AAG TGC CGA GCA TAT GCC AAA GCA							1968
45	Val Leu Leu Gly Glu Arg Ala Ala Lys Cys Arg Ala Tyr Ala Lys Ala							
		645		650			655	
	CTA CAC TAC AAA GAA CTG GAG TTC CAG AAA GGC CCC ACC CCT GCC ATT							2016
	Leu His Tyr Lys Glu Leu Glu Phe Gln Lys Gly Pro Thr Pro Ala Ile							
50		660		665			670	
	CTA GAA TCT CTC ATC AGC ATT AAT AAT AAG CTA CAG CAG CCG GAG GCA							2064
	Leu Glu Ser Leu Ile Ser Ile Asn Asn Lys Leu Gln Gln Pro Glu Ala							
		675		680			685	
55	GCG GCC GGA GTG TTA GAA TAT GCC ATG AAA CAC TTT GGA GAG CTG GAG							2112
	Ala Ala Gly Val Leu Glu Tyr Ala Met Lys His Phe Gly Glu Leu Glu							
		690		695			700	

	ATC	CAG	GCT	ACC	TGG	TAT	GAG	AAA	CTG	CAC	GAG	TGG	GAG	GAT	GCC	CTT	2160
	Ile	Gln	Ala	Thr	Trp	Tyr	Glu	Lys	Leu	His	Glu	Trp	Glu	Asp	Ala	Leu	
	705					710					715					720	
5	GTG	GCC	TAT	GAC	AAG	AAA	ATG	GAC	ACC	AAC	AAG	GAC	GAC	CCA	GAG	CTG	2208
	Val	Ala	Tyr	Asp	Lys	Lys	Met	Asp	Thr	Asn	Lys	Asp	Asp	Pro	Glu	Leu	
					725					730						735	
10	ATG	CTG	GGC	CGC	ATG	CGC	TGC	CTC	GAG	GCC	TTG	GGG	GAA	TGG	GGT	CAA	2256
	Met	Leu	Gly	Arg	Met	Arg	Cys	Leu	Glu	Ala	Leu	Gly	Glu	Trp	Gly	Gln	
				740						745						750	
15	CTC	CAC	CAG	CAG	TGC	TGT	GAA	AAG	TGG	ACC	CTG	GTT	AAT	GAT	GAG	ACC	2304
	Leu	His	Gln	Gln	Cys	Cys	Glu	Lys	Trp	Thr	Leu	Val	Asn	Asp	Glu	Thr	
			755						760							765	
20	CAA	GCC	AAG	ATG	GCC	CGG	ATG	GCT	GCT	GCA	GCT	GCA	TGG	GGT	TTA	GGT	2352
	Gln	Ala	Lys	Met	Ala	Arg	Met	Ala	Ala	Ala	Ala	Ala	Ala	Trp	Gly	Leu	
			770						775							780	
25	CAG	TGG	GAC	AGC	ATG	GAA	GAA	TAC	ACC	TGT	ATG	ATC	CCT	CGG	GAC	ACC	2400
	Gln	Trp	Asp	Ser	Met	Glu	Glu	Tyr	Thr	Cys	Met	Ile	Pro	Arg	Asp	Thr	
						785										800	
30	CAT	GAT	GGG	GCA	TTT	TAT	AGA	GCT	GTG	CTG	GCA	CTG	CAT	CAG	GAC	CTC	2448
	His	Asp	Gly	Ala	Phe	Tyr	Arg	Ala	Val	Leu	Ala	Leu	His	Gln	Asp	Leu	
					805											815	
35	TTC	TCC	TTG	GCA	CAA	CAG	TGC	ATT	GAC	AAG	GCC	AGG	GAC	CTG	CTG	GAT	2496
	Phe	Ser	Leu	Ala	Gln	Gln	Cys	Ile	Asp	Lys	Ala	Arg	Asp	Leu	Leu	Asp	
				820												830	
40	GCT	GAA	TTA	ACT	GCA	ATG	GCA	GGA	GAG	AGT	TAC	AGT	CGG	GCA	TAT	GGG	2544
	Ala	Glu	Leu	Thr	Ala	Met	Ala	Gly	Glu	Ser	Tyr	Ser	Arg	Ala	Tyr	Gly	
				835												845	
45	GCC	ATG	GTT	TCT	TGC	CAC	ATG	CTG	TCC	GAG	CTG	GAG	GAG	GTT	ATC	CAG	2592
	Ala	Met	Val	Ser	Cys	His	Met	Leu	Ser	Glu	Leu	Glu	Glu	Val	Ile	Gln	
				850												860	
50	TAC	AAA	CTT	GTC	CCC	GAG	CGA	CGA	GAG	ATC	ATC	CGC	CAG	ATC	TGG	TGG	2640
	Tyr	Lys	Leu	Val	Pro	Glu	Arg	Arg	Glu	Ile	Ile	Arg	Gln	Ile	Trp	Trp	
						865										880	
55	GAG	AGA	CTG	CAG	GGC	TGC	CAG	CGT	ATC	GTA	GAG	GAC	TGG	CAG	AAA	ATC	2688
	Glu	Arg	Leu	Gln	Gly	Cys	Gln	Arg	Ile	Val	Glu	Asp	Trp	Gln	Lys	Ile	
					885											895	
60	CTT	ATG	GTG	CGG	TCC	CTT	GTG	GTC	AGC	CCT	CAT	GAA	GAC	ATG	AGA	ACC	2736
	Leu	Met	Val	Arg	Ser	Leu	Val	Val	Ser	Pro	His	Glu	Asp	Met	Arg	Thr	
				900												910	
65	TGG	CTC	AAG	TAT	GCA	AGC	CTG	TGC	GGC	AAG	AGT	GGC	AGG	CTG	GCT	CTT	2784
	Trp	Leu	Lys	Tyr	Ala	Ser	Leu	Cys	Gly	Lys	Ser	Gly	Arg	Leu	Ala	Leu	
				915												925	
70	GCT	CAT	AAA	ACT	TTA	GTG	TTG	CTC	CTG	GGA	GTT	GAT	CCG	TCT	CGG	CAA	2832
	Ala	His	Lys	Thr	Leu	Val	Leu	Leu	Leu	Gly	Val	Asp	Pro	Ser	Arg	Gln	

	930	935	940	
5	CTT GAC CAT CCT CTG CCA ACA GTT CAC CCT CAG GTG ACC TAT GCC TAC Leu Asp His Pro Leu Pro Thr Val His Pro Gln Val Thr Tyr Ala Tyr 945 950 955 960			2880
10	ATG AAA AAC ATG TGG AAG AGT GCC CGC AAG ATC GAT GCC TTC CAG CAC Met Lys Asn Met Trp Lys Ser Ala Arg Lys Ile Asp Ala Phe Gln His 965 970 975			2928
15	ATG CAG CAT TTT GTC CAG ACC ATG CAG CAA CAG GCC CAG CAT GCC ATC Met Gln His Phe Val Gln Thr Met Gln Gln Gln Ala Gln His Ala Ile 980 985 990			2976
20	GCT ACT GAG GAC CAG CAG CAT AAG CAG GAA CTG CAC AAG CTC ATG GCC Ala Thr Glu Asp Gln Gln His Lys Gln Glu Leu His Lys Leu Met Ala 995 1000 1005			3024
25	CGA TGC TTC CTG AAA CTT GGA GAG TGG CAG CTG AAT CTA CAG GGC ATC Arg Cys Phe Leu Lys Leu Gly Glu Trp Gln Leu Asn Leu Gln Gly Ile 1010 1015 1020			3072
30	AAT GAG AGC ACA ATC CCC AAA GTG CTG CAG TAC TAC AGC GCC GCC ACA Asn Glu Ser Thr Ile Pro Lys Val Leu Gln Tyr Tyr Ser Ala Ala Thr 1025 1030 1035 1040			3120
35	GAG CAC GAC CGC AGC TGG TAC AAG GCC TGG CAT GCG TGG GCA GTG ATG Glu His Asp Arg Ser Trp Tyr Lys Ala Trp His Ala Trp Ala Val Met 1045 1050 1055			3168
40	AAC TTC GAA GCT GTG CTA CAC TAC AAA CAT CAG AAC CAA GCC CGC GAT Asn Phe Glu Ala Val Leu His Tyr Lys His Gln Asn Gln Ala Arg Asp 1060 1065 1070			3216
45	GAG AAG AAG AAA CTG CGT CAT GCC AGC GGG GCC AAC ATC ACC AAC GCC Glu Lys Lys Lys Leu Arg His Ala Ser Gly Ala Asn Ile Thr Asn Ala 1075 1080 1085			3264
50	ACC ACT GCC GCC ACC ACG GCC GCC ACT GCC ACC ACC ACT GCC AGC ACC Thr Thr Ala Ala Thr Thr Ala Ala Thr Ala Thr Thr Thr Ala Ser Thr 1090 1095 1100			3312
55	GAG GGC AGC AAC AGT GAG AGC GAG GCC GAG AGC ACC GAG AAC AGC CCC Glu Gly Ser Asn Ser Glu Ser Glu Ala Glu Ser Thr Glu Asn Ser Pro 1105 1110 1115 1120			3360
60	ACC CCA TCG CCG CTG CAG AAG AAG GTC ACT GAG GAT CTG TCC AAA ACC Thr Pro Ser Pro Leu Gln Lys Lys Val Thr Glu Asp Leu Ser Lys Thr 1125 1130 1135			3408
65	CTC CTG ATG TAC ACG GTG CCT GCC GTC CAG GGC TTC TTC CGT TCC ATC Leu Leu Met Tyr Thr Val Pro Ala Val Gln Gly Phe Phe Arg Ser Ile 1140 1145 1150			3456
70	TCC TTG TCA CGA GGC AAC AAC CTC CAG GAT ACA CTC AGA GTT CTC ACC Ser Leu Ser Arg Gly Asn Asn Leu Gln Asp Thr Leu Arg Val Leu Thr 1155 1160 1165			3504

	TTA TGG TTT GAT TAT GGT CAC TGG CCA GAT GTC AAT GAG GCC TTA GTG	3552
	Leu Trp Phe Asp Tyr Gly His Trp Pro Asp Val Asn Glu Ala Leu Val	
	1170 1175 1180	
5	GAG GGG GTG AAA GCC ATC CAG ATT GAT ACC TGG CTA CAG GTT ATA CCT	3600
	Glu Gly Val Lys Ala Ile Gln Ile Asp Thr Trp Leu Gln Val Ile Pro	
	1185 1190 1195 1200	
10	CAG CTC ATT GCA AGA ATT GAT ACG CCC AGA CCC TTG GTG GGA CGT CTC	3648
	Gln Leu Ile Ala Arg Ile Asp Thr Pro Arg Pro Leu Val Gly Arg Leu	
	1205 1210 1215	
15	ATT CAC CAG CTT CTC ACA GAC ATT GGT CGG TAC CAC CCC CAG GCC CTC	3696
	Ile His Gln Leu Leu Thr Asp Ile Gly Arg Tyr His Pro Gln Ala Leu	
	1220 1225 1230	
20	ATC TAC CCA CTG ACA GTG GCT TCT AAG TCT ACC ACG ACA GCC CGG CAC	3744
	Ile Tyr Pro Leu Thr Val Ala Ser Lys Ser Thr Thr Thr Ala Arg His	
	1235 1240 1245	
25	AAT GCA GCC AAC AAG ATT CTG AAG AAC ATG TGT GAG CAC AGC AAC ACC	3792
	Asn Ala Ala Asn Lys Ile Leu Lys Asn Met Cys Glu His Ser Asn Thr	
	1250 1255 1260	
30	CTG GTC CAG CAG GCC ATG ATG GTG AGC GAG GAG CTG ATC CGA GTG GCC	3840
	Leu Val Gln Gln Ala Met Met Val Ser Glu Glu Leu Ile Arg Val Ala	
	1265 1270 1275 1280	
35	ATC CTC TGG CAT GAG ATG TGG CAT GAA GGC CTG GAA GAG GCA TCT CGT	3888
	Ile Leu Trp His Glu Met Trp His Glu Gly Leu Glu Glu Ala Ser Arg	
	1285 1290 1295	
40	TTG TAC TTT GGG GAA AGG AAC GTG AAA GGC ATG TTT GAG GTG CTG GAG	3936
	Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly Met Phe Glu Val Leu Glu	
	1300 1305 1310	
45	CCC TTG CAT GCT ATG ATG GAA CGG GGC CCC CAG ACT CTG AAG GAA ACA	3984
	Pro Leu His Ala Met Met Glu Arg Gly Pro Gln Thr Leu Lys Glu Thr	
	1315 1320 1325	
50	TCC TTT AAT CAG GCC TAT GGT CGA GAT TTA ATG GAG GCC CAA GAG TGG	4032
	Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu Ala Gln Glu Trp	
	1330 1335 1340	
55	TGC AGG AAG TAC ATG AAA TCA GGG AAT GTC AAG GAC CTC ACC CAA GCC	4080
	Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp Leu Thr Gln Ala	
	1345 1350 1355 1360	
60	TGG GAC CTC TAT TAT CAT GTG TTC CGA CGA ATC TCA AAG CAG CTG CCT	4128
	Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser Lys Gln Leu Pro	
	1365 1370 1375	
65	CAG CTC ACA TCC TTA GAG CTG CAA TAT GTT TCC CCA AAA CTT CTG ATG	4176
	Gln Leu Thr Ser Leu Glu Leu Gln Tyr Val Ser Pro Lys Leu Leu Met	
	1380 1385 1390	
70	TGC CGG GAC CTT GAA TTG GCT GTG CCA GGA ACA TAT GAC CCC AAC CAG	4224
	Cys Arg Asp Leu Glu Leu Ala Val Pro Gly Thr Tyr Asp Pro Asn Gln	

	1395	1400	1405	
5	CCA ATC ATT CGC ATT CAG TCC ATA GCA CCG TCT TTG CAA GTC ATC ACA Pro Ile Ile Arg Ile Gln Ser Ile Ala Pro Ser Leu Gln Val Ile Thr 1410 1415 1420			4272
10	TCC AAG CAG AGG CCC CGG AAA TTG ACA CTT ATG GGC AGC AAC GGA CAT Ser Lys Gln Arg Pro Arg Lys Leu Thr Leu Met Gly Ser Asn Gly His 1425 1430 1435 1440			4320
	GAG TTT GTT TTC CTT CTA AAA GGC CAT GAA GAT CTG CGC CAG GAT GAG Glu Phe Val Phe Leu Leu Lys Gly His Glu Asp Leu Arg Gln Asp Glu 1445 1450 1455			4368
15	CGT GTG ATG CAG CTC TTC GGC CTG GTT AAC ACC CTT CTG GCC AAT GAC Arg Val Met Gln Leu Phe Gly Leu Val Asn Thr Leu Leu Ala Asn Asp 1460 1465 1470			4416
20	CCA ACA TCT CTT CGG AAA AAC CTC AGC ATC CAG AGA TAC GCT GTC ATC Pro Thr Ser Leu Arg Lys Asn Leu Ser Ile Gln Arg Tyr Ala Val Ile 1475 1480 1485			4464
25	CCT TTA TCG ACC AAC TCG GGC CTC ATT GGC TGG GTT CCC CAC TGT GAC Pro Leu Ser Thr Asn Ser Gly Leu Ile Gly Trp Val Pro His Cys Asp 1490 1495 1500			4512
30	ACA CTG CAC GCC CTC ATC CGG GAC TAC AGG GAG AAG AAG AAG ATC CTT Thr Leu His Ala Leu Ile Arg Asp Tyr Arg Glu Lys Lys Lys Ile Leu 1505 1510 1515 1520			4560
	CTC AAC ATC GAG CAT CGC ATC ATG TTG CGG ATG GCT CCG GAC TAT GAC Leu Asn Ile Glu His Arg Ile Met Leu Arg Met Ala Pro Asp Tyr Asp 1525 1530 1535			4608
35	CAC TTG ACT CTG ATG CAG AAG GTG GAG GTG TTT GAG CAT GCC GTC AAT His Leu Thr Leu Met Gln Lys Val Glu Val Phe Glu His Ala Val Asn 1540 1545 1550			4656
40	AAT ACA GCT GGG GAC GAC CTG GCC AAG CTG CTG TGG CTG AAA AGC CCC Asn Thr Ala Gly Asp Asp Leu Ala Lys Leu Leu Trp Leu Lys Ser Pro 1555 1560 1565			4704
45	AGC TCC GAG GTG TGG TTT GAC CGA AGA ACC AAT TAT ACC CGT TCT TTA Ser Ser Glu Val Trp Phe Asp Arg Arg Thr Asn Tyr Thr Arg Ser Leu 1570 1575 1580			4752
50	GCG GTC ATG TCA ATG GTT GGG TAT ATT TTA GGC CTG GGA GAT AGA CAC Ala Val Met Ser Met Val Gly Tyr Ile Leu Gly Leu Gly Asp Arg His 1585 1590 1595 1600			4800
	CCA TCC AAC CTG ATG CTG GAC CGT CTG AGT GGG AAG ATC CTG CAC ATT Pro Ser Asn Leu Met Leu Asp Arg Leu Ser Gly Lys Ile Leu His Ile 1605 1610 1615			4848
55	GAC TTT GGG GAC TGC TTT GAG GTT GCT ATG ACC CGA GAG AAG TTT CCA Asp Phe Gly Asp Cys Phe Glu Val Ala Met Thr Arg Glu Lys Phe Pro 1620 1625 1630			4896

	GAG AAG ATT CCA TTT AGA CTA ACA AGA ATG TTG ACC AAT GCT ATG GAG	4944
	Glu Lys Ile Pro Phe Arg Leu Thr Arg Met Leu Thr Asn Ala Met Glu	
	1635 1640 1645	
5	GTT ACA GGC CTG GAT GGC AAC TAC AGA ATC ACA TGC CAC ACA GTG ATG	4992
	Val Thr Gly Leu Asp Gly Asn Tyr Arg Ile Thr Cys His Thr Val Met	
	1650 1655 1660	
10	GAG GTG CTG CGA GAG CAC AAG GAC AGT GTC ATG GCC GTG CTG GAA GCC	5040
	Glu Val Leu Arg Glu His Lys Asp Ser Val Met Ala Val Leu Glu Ala	
	1665 1670 1675 1680	
15	TTT GTC TAT GAC CCC TTG CTG AAC TGG AGG CTG ATG GAC ACA AAT ACC	5088
	Phe Val Tyr Asp Pro Leu Leu Asn Trp Arg Leu Met Asp Thr Asn Thr	
	1685 1690 1695	
20	AAA GGC AAC AAG CGA TCC CGA ACG AGG ACG GAT TCC TAC TCT GCT GGC	5136
	Lys Gly Asn Lys Arg Ser Arg Thr Arg Thr Asp Ser Tyr Ser Ala Gly	
	1700 1705 1710	
25	CAG TCA GTC GAA ATT TTG GAC GGT GTG GAA CTT GGA GAG CCA GCC CAT	5184
	Gln Ser Val Glu Ile Leu Asp Gly Val Glu Leu Gly Glu Pro Ala His	
	1715 1720 1725	
30	AAG AAA ACG GGG ACC ACA GTG CCA GAA TCT ATT CAT TCT TTC ATT GGA	5232
	Lys Lys Thr Gly Thr Thr Val Pro Glu Ser Ile His Ser Phe Ile Gly	
	1730 1735 1740	
35	GAC GGT TTG GTG AAA CCA GAG GCC CTA AAT AAG AAA GCT ATC CAG ATT	5280
	Asp Gly Leu Val Lys Pro Glu Ala Leu Asn Lys Lys Ala Ile Gln Ile	
	1745 1750 1755 1760	
40	ATT AAC AGG GTT CGA GAT AAG CTC ACT GGT CGG GAC TTC TCT CAT GAT	5328
	Ile Asn Arg Val Arg Asp Lys Leu Thr Gly Arg Asp Phe Ser His Asp	
	1765 1770 1775	
45	GAC ACT TTG GAT GTT CCA ACG CAA GTT GAG CTG CTC ATC AAA CAA GCG	5376
	Asp Thr Leu Asp Val Pro Thr Gln Val Glu Leu Leu Ile Lys Gln Ala	
	1780 1785 1790	
50	ACA TCC CAT GAA AAC CTC TGC CAG TGC TAT ATT GGC TGG TGC CCT TTC	5424
	Thr Ser His Glu Asn Leu Cys Gln Cys Tyr Ile Gly Trp Cys Pro Phe	
	1795 1800 1805	
55	TGG TAA	5430
	Trp	

50 (2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1809 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

	Leu	Glu	His	Ser	Gly	Ile	Gly	Arg	Ile	Lys	Glu	Gln	Ser	Ala	Arg	Met	
	1				5					10					15		
5	Leu	Gly	His	Leu	Val	Ser	Asn	Ala	Pro	Arg	Leu	Ile	Arg	Pro	Tyr	Met	
				20					25					30			
	Glu	Pro	Ile	Leu	Lys	Ala	Leu	Ile	Leu	Lys	Leu	Lys	Asp	Pro	Asp	Pro	
10				35				40					45				
	Asp	Pro	Asn	Pro	Gly	Val	Ile	Asn	Asn	Val	Leu	Ala	Thr	Ile	Gly	Glu	
		50					55					60					
15	Leu	Ala	Gln	Val	Ser	Gly	Leu	Glu	Met	Arg	Lys	Trp	Val	Asp	Glu	Leu	
	65					70					75					80	
	Phe	Ile	Ile	Ile	Met	Asp	Met	Leu	Gln	Asp	Ser	Ser	Leu	Leu	Ala	Lys	
					85				90						95		
20	Arg	Gln	Val	Ala	Leu	Trp	Thr	Leu	Gly	Gln	Leu	Val	Ala	Ser	Thr	Gly	
				100					105					110			
	Tyr	Val	Val	Glu	Pro	Tyr	Arg	Lys	Tyr	Pro	Thr	Leu	Leu	Glu	Val	Leu	
25				115				120					125				
	Leu	Asn	Phe	Leu	Lys	Thr	Glu	Gln	Asn	Gln	Gly	Thr	Arg	Arg	Glu	Ala	
		130					135					140					
30	Ile	Arg	Val	Leu	Gly	Leu	Leu	Gly	Ala	Leu	Asp	Pro	Tyr	Lys	His	Lys	
	145					150					155					160	
	Val	Asn	Ile	Gly	Met	Ile	Asp	Gln	Ser	Arg	Asp	Ala	Ser	Ala	Val	Ser	
				165					170						175		
35	Leu	Ser	Glu	Ser	Lys	Ser	Ser	Gln	Asp	Ser	Ser	Asp	Tyr	Ser	Thr	Ser	
				180					185					190			
	Glu	Met	Leu	Val	Asn	Met	Gly	Asn	Leu	Pro	Leu	Asp	Glu	Phe	Tyr	Pro	
40				195				200					205				
	Ala	Val	Ser	Met	Val	Ala	Leu	Met	Arg	Ile	Phe	Arg	Asp	Gln	Ser	Leu	
		210					215					220					
45	Ser	His	His	His	Thr	Met	Val	Val	Gln	Ala	Ile	Thr	Phe	Ile	Phe	Lys	
	225					230					235					240	
	Ser	Leu	Gly	Leu	Lys	Cys	Val	Gln	Phe	Leu	Pro	Gln	Val	Met	Pro	Thr	
				245						250				255			
50	Phe	Leu	Asn	Val	Ile	Arg	Val	Cys	Asp	Gly	Ala	Ile	Arg	Glu	Phe	Leu	
				260					265					270			
	Phe	Gln	Gln	Leu	Gly	Met	Leu	Val	Ser	Phe	Val	Lys	Ser	His	Ile	Arg	
55				275				280					285				
	Pro	Tyr	Met	Asp	Glu	Ile	Val	Thr	Leu	Met	Arg	Glu	Phe	Trp	Val	Met	
		290					295						300				

	Asn Thr Ser Ile Gln Ser Thr Ile Ile Leu Leu Ile Glu Gln Ile Val	
	305	310 315 320
5	Val Ala Leu Gly Gly Glu Phe Lys Leu Tyr Leu Pro Gln Leu Ile Pro	
		325 330 335
	His Met Leu Arg Val Phe Met His Asp Asn Ser Pro Gly Arg Ile Val	
		340 345 350
10	Ser Ile Lys Leu Leu Ala Ala Ile Gln Leu Phe Gly Ala Asn Leu Asp	
		355 360 365
	Asp Tyr Leu His Leu Leu Leu Pro Pro Ile Val Lys Leu Phe Asp Ala	
15		370 375 380
	Pro Glu Ala Pro Leu Pro Ser Arg Lys Ala Ala Leu Glu Thr Val Asp	
		385 390 395 400
20	Arg Leu Thr Glu Ser Leu Asp Phe Thr Asp Tyr Ala Ser Arg Ile Ile	
		405 410 415
	His Pro Ile Val Arg Thr Leu Asp Gln Ser Pro Glu Leu Arg Ser Thr	
		420 425 430
25	Ala Met Asp Thr Leu Ser Ser Leu Val Phe Gln Leu Gly Lys Lys Tyr	
		435 440 445
	Gln Ile Phe Ile Pro Met Val Asn Lys Val Leu Val Arg His Arg Ile	
30		450 455 460
	Asn His Gln Arg Tyr Asp Val Leu Ile Cys Arg Ile Val Lys Gly Tyr	
		465 470 475 480
35	Thr Leu Ala Asp Glu Glu Glu Asp Pro Leu Ile Tyr Gln His Arg Met	
		485 490 495
	Leu Arg Ser Gly Gln Gly Asp Ala Leu Ala Ser Gly Pro Val Glu Thr	
		500 505 510
40	Gly Pro Met Lys Lys Leu His Val Ser Thr Ile Asn Leu Gln Lys Ala	
		515 520 525
	Trp Gly Ala Ala Arg Arg Val Ser Lys Asp Asp Trp Leu Glu Trp Leu	
45		530 535 540
	Arg Arg Leu Ser Leu Glu Leu Leu Lys Asp Ser Ser Ser Pro Ser Leu	
		545 550 555 560
50	Arg Ser Cys Trp Ala Leu Ala Gln Ala Tyr Asn Pro Met Ala Arg Asp	
		565 570 575
	Leu Phe Asn Ala Ala Phe Val Ser Cys Trp Ser Glu Leu Asn Glu Asp	
		580 585 590
55	Gln Gln Asp Glu Leu Ile Arg Ser Ile Glu Leu Ala Leu Thr Ser Gln	
		595 600 605

	Asp	Ile	Ala	Glu	Val	Thr	Gln	Thr	Leu	Leu	Asn	Leu	Ala	Glu	Phe	Met	
	610						615					620					
5	Glu	His	Ser	Asp	Lys	Gly	Pro	Leu	Pro	Leu	Arg	Asp	Asp	Asn	Gly	Ile	
	625					630					635					640	
	Val	Leu	Leu	Gly	Glu	Arg	Ala	Ala	Lys	Cys	Arg	Ala	Tyr	Ala	Lys	Ala	
				645						650					655		
10	Leu	His	Tyr	Lys	Glu	Leu	Glu	Phe	Gln	Lys	Gly	Pro	Thr	Pro	Ala	Ile	
				660					665					670			
	Leu	Glu	Ser	Leu	Ile	Ser	Ile	Asn	Asn	Lys	Leu	Gln	Gln	Pro	Glu	Ala	
			675					680					685				
15	Ala	Ala	Gly	Val	Leu	Glu	Tyr	Ala	Met	Lys	His	Phe	Gly	Glu	Leu	Glu	
			690				695					700					
	Ile	Gln	Ala	Thr	Trp	Tyr	Glu	Lys	Leu	His	Glu	Trp	Glu	Asp	Ala	Leu	
20	705					710					715				720		
	Val	Ala	Tyr	Asp	Lys	Lys	Met	Asp	Thr	Asn	Lys	Asp	Asp	Pro	Glu	Leu	
				725						730					735		
25	Met	Leu	Gly	Arg	Met	Arg	Cys	Leu	Glu	Ala	Leu	Gly	Glu	Trp	Gly	Gln	
				740				745						750			
	Leu	His	Gln	Gln	Cys	Cys	Glu	Lys	Trp	Thr	Leu	Val	Asn	Asp	Glu	Thr	
			755					760					765				
30	Gln	Ala	Lys	Met	Ala	Arg	Met	Ala	Ala	Ala	Ala	Ala	Trp	Gly	Leu	Gly	
		770					775					780					
	Gln	Trp	Asp	Ser	Met	Glu	Glu	Tyr	Thr	Cys	Met	Ile	Pro	Arg	Asp	Thr	
35	785					790					795				800		
	His	Asp	Gly	Ala	Phe	Tyr	Arg	Ala	Val	Leu	Ala	Leu	His	Gln	Asp	Leu	
				805						810				815			
40	Phe	Ser	Leu	Ala	Gln	Gln	Cys	Ile	Asp	Lys	Ala	Arg	Asp	Leu	Leu	Asp	
			820					825						830			
	Ala	Glu	Leu	Thr	Ala	Met	Ala	Gly	Glu	Ser	Tyr	Ser	Arg	Ala	Tyr	Gly	
			835					840					845				
45	Ala	Met	Val	Ser	Cys	His	Met	Leu	Ser	Glu	Leu	Glu	Glu	Val	Ile	Gln	
		850					855					860					
	Tyr	Lys	Leu	Val	Pro	Glu	Arg	Arg	Glu	Ile	Ile	Arg	Gln	Ile	Trp	Trp	
50	865					870					875				880		
	Glu	Arg	Leu	Gln	Gly	Cys	Gln	Arg	Ile	Val	Glu	Asp	Trp	Gln	Lys	Ile	
				885					890					895			
55	Leu	Met	Val	Arg	Ser	Leu	Val	Val	Ser	Pro	His	Glu	Asp	Met	Arg	Thr	
			900					905						910			
	Trp	Leu	Lys	Tyr	Ala	Ser	Leu	Cys	Gly	Lys	Ser	Gly	Arg	Leu	Ala	Leu	

	915	920	925
	Ala His Lys Thr Leu Val	Leu Leu Leu Gly Val	Asp Pro Ser Arg Gln
	930	935	940
5	Leu Asp His Pro Leu Pro Thr Val His Pro Gln Val Thr Tyr Ala Tyr		
	945	950	955 960
10	Met Lys Asn Met Trp Lys Ser Ala Arg Lys Ile Asp Ala Phe Gln His		
		965	970 975
	Met Gln His Phe Val Gln Thr Met Gln Gln Gln Ala Gln His Ala Ile		
		980	985 990
15	Ala Thr Glu Asp Gln Gln His Lys Gln Glu Leu His Lys Leu Met Ala		
		995	1000 1005
	Arg Cys Phe Leu Lys Leu Gly Glu Trp Gln Leu Asn Leu Gln Gly Ile		
		1010	1015 1020
20	Asn Glu Ser Thr Ile Pro Lys Val Leu Gln Tyr Tyr Ser Ala Ala Thr		
		1025	1030 1035 1040
	Glu His Asp Arg Ser Trp Tyr Lys Ala Trp His Ala Trp Ala Val Met		
		1045	1050 1055
25	Asn Phe Glu Ala Val Leu His Tyr Lys His Gln Asn Gln Ala Arg Asp		
		1060	1065 1070
30	Glu Lys Lys Lys Leu Arg His Ala Ser Gly Ala Asn Ile Thr Asn Ala		
		1075	1080 1085
	Thr Thr Ala Ala Thr Thr Ala Ala Thr Ala Thr Thr Thr Ala Ser Thr		
		1090	1095 1100
35	Glu Gly Ser Asn Ser Glu Ser Glu Ala Glu Ser Thr Glu Asn Ser Pro		
		1105	1110 1115 1120
	Thr Pro Ser Pro Leu Gln Lys Lys Val Thr Glu Asp Leu Ser Lys Thr		
		1125	1130 1135
40	Leu Leu Met Tyr Thr Val Pro Ala Val Gln Gly Phe Phe Arg Ser Ile		
		1140	1145 1150
	Ser Leu Ser Arg Gly Asn Asn Leu Gln Asp Thr Leu Arg Val Leu Thr		
		1155	1160 1165
	Leu Trp Phe Asp Tyr Gly His Trp Pro Asp Val Asn Glu Ala Leu Val		
		1170	1175 1180
50	Glu Gly Val Lys Ala Ile Gln Ile Asp Thr Trp Leu Gln Val Ile Pro		
		1185	1190 1195 1200
	Gln Leu Ile Ala Arg Ile Asp Thr Pro Arg Pro Leu Val Gly Arg Leu		
		1205	1210 1215
55	Ile His Gln Leu Leu Thr Asp Ile Gly Arg Tyr His Pro Gln Ala Leu		
		1220	1225 1230

Ile Tyr Pro Leu Thr Val Ala Ser Lys Ser Thr Thr Thr Ala Arg His
1235 1240 1245

5 Asn Ala Ala Asn Lys Ile Leu Lys Asn Met Cys Glu His Ser Asn Thr
1250 1255 1260

Leu Val Gln Gln Ala Met Met Val Ser Glu Glu Leu Ile Arg Val Ala
1265 1270 1275 1280

10 Ile Leu Trp His Glu Met Trp His Glu Gly Leu Glu Glu Ala Ser Arg
1285 1290 1295

Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly Met Phe Glu Val Leu Glu
15 1300 1305 1310

Pro Leu His Ala Met Met Glu Arg Gly Pro Gln Thr Leu Lys Glu Thr
1315 1320 1325

20 Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu Ala Gln Glu Trp
1330 1335 1340

Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp Leu Thr Gln Ala
1345 1350 1355 1360

25 Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser Lys Gln Leu Pro
1365 1370 1375

Gln Leu Thr Ser Leu Glu Leu Gln Tyr Val Ser Pro Lys Leu Leu Met
30 1380 1385 1390

Cys Arg Asp Leu Glu Leu Ala Val Pro Gly Thr Tyr Asp Pro Asn Gln
1395 1400 1405

35 Pro Ile Ile Arg Ile Gln Ser Ile Ala Pro Ser Leu Gln Val Ile Thr
1410 1415 1420

Ser Lys Gln Arg Pro Arg Lys Leu Thr Leu Met Gly Ser Asn Gly His
1425 1430 1435 1440

40 Glu Phe Val Phe Leu Leu Lys Gly His Glu Asp Leu Arg Gln Asp Glu
1445 1450 1455

Arg Val Met Gln Leu Phe Gly Leu Val Asn Thr Leu Leu Ala Asn Asp
45 1460 1465 1470

Pro Thr Ser Leu Arg Lys Asn Leu Ser Ile Gln Arg Tyr Ala Val Ile
1475 1480 1485

50 Pro Leu Ser Thr Asn Ser Gly Leu Ile Gly Trp Val Pro His Cys Asp
1490 1495 1500

Thr Leu His Ala Leu Ile Arg Asp Tyr Arg Glu Lys Lys Lys Ile Leu
1505 1510 1515 1520

55 Leu Asn Ile Glu His Arg Ile Met Leu Arg Met Ala Pro Asp Tyr Asp
1525 1530 1535

His Leu Thr Leu Met Gln Lys Val Glu Val Phe Glu His Ala Val Asn
 1540 1545 1550
 5 Asn Thr Ala Gly Asp Asp Leu Ala Lys Leu Leu Trp Leu Lys Ser Pro
 1555 1560 1565
 Ser Ser Glu Val Trp Phe Asp Arg Arg Thr Asn Tyr Thr Arg Ser Leu
 1570 1575 1580
 10 Ala Val Met Ser Met Val Gly Tyr Ile Leu Gly Leu Gly Asp Arg His
 1585 1590 1595 1600
 Pro Ser Asn Leu Met Leu Asp Arg Leu Ser Gly Lys Ile Leu His Ile
 1605 1610 1615
 15 Asp Phe Gly Asp Cys Phe Glu Val Ala Met Thr Arg Glu Lys Phe Pro
 1620 1625 1630
 Glu Lys Ile Pro Phe Arg Leu Thr Arg Met Leu Thr Asn Ala Met Glu
 20 1635 1640 1645
 Val Thr Gly Leu Asp Gly Asn Tyr Arg Ile Thr Cys His Thr Val Met
 1650 1655 1660
 25 Glu Val Leu Arg Glu His Lys Asp Ser Val Met Ala Val Leu Glu Ala
 1665 1670 1675 1680
 Phe Val Tyr Asp Pro Leu Leu Asn Trp Arg Leu Met Asp Thr Asn Thr
 1685 1690 1695
 30 Lys Gly Asn Lys Arg Ser Arg Thr Arg Thr Asp Ser Tyr Ser Ala Gly
 1700 1705 1710
 Gln Ser Val Glu Ile Leu Asp Gly Val Glu Leu Gly Glu Pro Ala His
 35 1715 1720 1725
 Lys Lys Thr Gly Thr Thr Val Pro Glu Ser Ile His Ser Phe Ile Gly
 1730 1735 1740
 40 Asp Gly Leu Val Lys Pro Glu Ala Leu Asn Lys Lys Ala Ile Gln Ile
 1745 1750 1755 1760
 Ile Asn Arg Val Arg Asp Lys Leu Thr Gly Arg Asp Phe Ser His Asp
 1765 1770 1775
 45 Asp Thr Leu Asp Val Pro Thr Gln Val Glu Leu Leu Ile Lys Gln Ala
 1780 1785 1790
 Thr Ser His Glu Asn Leu Cys Gln Cys Tyr Ile Gly Trp Cys Pro Phe
 50 1795 1800 1805
 Trp

55

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1794 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

10

(A) NAME/KEY: CDS

(B) LOCATION: 1..1686

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

15

TTG GTT TAC CCT TTG ACA GTT GCT ATT ACT TCC GAA TCA ACG AGC CGT	48
Leu Val Tyr Pro Leu Thr Val Ala Ile Thr Ser Glu Ser Thr Ser Arg	
1 5 10 15	

20

AAA AAG GCA GCT CAA TCC ATT ATT GAA AAA ATG CGA GTA CAT TCT CCT	96
Lys Lys Ala Ala Gln Ser Ile Ile Glu Lys Met Arg Val His Ser Pro	
20 25 30	

25

AGC TTG GTG GAT CAA GCA GAA TTA GTG AGT CGA GAA CTC ATC CGA GTT	144
Ser Leu Val Asp Gln Ala Glu Leu Val Ser Arg Glu Leu Ile Arg Val	
35 40 45	

30

GCA GTT TTA TGG CAC GAA CAA TGG CAC GAT GCT TTG GAA GAT GCT AGC	192
Ala Val Leu Trp His Glu Gln Trp His Asp Ala Leu Glu Asp Ala Ser	
50 55 60	

35

AGG TTT TTC TTT GGT GAA CAC AAC ACA GAA AAG ATG TTT GAA ACA TTG	240
Arg Phe Phe Phe Gly Glu His Asn Thr Glu Lys Met Phe Glu Thr Leu	
65 70 75 80	

40

GAA CCA TTA CAT CAA ATG TTG CAA AAG GGA CCA GAA ACG ATG AGG GAA	288
Glu Pro Leu His Gln Met Leu Gln Lys Gly Pro Glu Thr Met Arg Glu	
85 90 95	

45

CAA GCC TTT GCA AAT GCT TTT GGC AGG GAG TTG ACA GAT GCA TAC GAG	336
Gln Ala Phe Ala Asn Ala Phe Gly Arg Glu Leu Thr Asp Ala Tyr Glu	
100 105 110	

50

TGG GTG CTC AAC TTT AGA AGA ACT AAA GAC ATA ACC AAT TTG AAT CAA	384
Trp Val Leu Asn Phe Arg Arg Thr Lys Asp Ile Thr Asn Leu Asn Gln	
115 120 125	

55

GCA TGG GAT ATA TAC TAC AAT GTC TTT AGA AGA GTA AGC AAA CAG GTG	432
Ala Trp Asp Ile Tyr Tyr Asn Val Phe Arg Arg Val Ser Lys Gln Val	
130 135 140	

CAG CTG TTA GCT AGT CTT GAG TTG CAG TAT GTA TCT CCG GAC TTA GAG	480
Gln Leu Leu Ala Ser Leu Glu Leu Gln Tyr Val Ser Pro Asp Leu Glu	
145 150 155 160	

CAT GCT CAA GAT TTG GAA TTG GCT GTA CCA GGT ACT TAC CAA GCA GGC	528
His Ala Gln Asp Leu Glu Leu Ala Val Pro Gly Thr Tyr Gln Ala Gly	
165 170 175	

	AAA CCT GTG ATC AGA ATA ATC AAA TTT GAT CCT ACT TTT TCG ATT ATT	576
	Lys Pro Val Ile Arg Ile Ile Lys Phe Asp Pro Thr Phe Ser Ile Ile	
	180 185 190	
5	TCA TCT AAA CAA AGA CCG AGA AAA TTA TCG TGC AGA GGA AGT GAT GGT	624
	Ser Ser Lys Gln Arg Pro Arg Lys Leu Ser Cys Arg Gly Ser Asp Gly	
	195 200 205	
10	AAA GAC TAC CAA TAT GCG TTG AAA GGA CAT GAA GAT ATC AGA CAA GAT	672
	Lys Asp Tyr Gln Tyr Ala Leu Lys Gly His Glu Asp Ile Arg Gln Asp	
	210 215 220	
15	AAC TTA GTG ATG CAA TTG TTT GGT TTG GTT AAT ACG TTG TTG GTA AAT	720
	Asn Leu Val Met Gln Leu Phe Gly Leu Val Asn Thr Leu Leu Val Asn	
	225 230 235 240	
20	GAT CCG GTA TGT TTC AAG AGA CAT TTG GAT ATA CAA CAA TAT CCT GCT	768
	Asp Pro Val Cys Phe Lys Arg His Leu Asp Ile Gln Gln Tyr Pro Ala	
	245 250 255	
25	ATT CCA TTA TCA CCA AAA GTG GGA TTG CTT GGT TGG GTT CCA AAT AGT	816
	Ile Pro Leu Ser Pro Lys Val Gly Leu Leu Gly Trp Val Pro Asn Ser	
	260 265 270	
30	GAC ACT TTC CAT GTA TTG ATC AAA GGC TAT CGC GAA TCA AGA AGT ATA	864
	Asp Thr Phe His Val Leu Ile Lys Gly Tyr Arg Glu Ser Arg Ser Ile	
	275 280 285	
35	ATG TTG AAT ATT GAA CAC AGG CTT TTG TTG CAA ATG GCA CCT GAT TAT	912
	Met Leu Asn Ile Glu His Arg Leu Leu Leu Gln Met Ala Pro Asp Tyr	
	290 295 300	
40	GAT TTC TTG ACA TTA TTG CAA AAA GTT GAA GTG TTC ACA AGT GCA ATG	960
	Asp Phe Leu Thr Leu Leu Gln Lys Val Glu Val Phe Thr Ser Ala Met	
	305 310 315 320	
45	GAT AAT TGT AAG GGA CAG GAT TTG TAC AAA GTG TTA TGG CTC AAA TCT	1008
	Asp Asn Cys Lys Gly Gln Asp Leu Tyr Lys Val Leu Trp Leu Lys Ser	
	325 330 335	
50	AAA TCA TCC GAG GCG TGG TTG GAC CGT AGA ACA ACA TAC ACG AGA TCA	1056
	Lys Ser Ser Glu Ala Trp Leu Asp Arg Arg Thr Thr Tyr Thr Arg Ser	
	340 345 350	
55	TTA GCT GTA ATG TCT ATG GTT GGG TAT ATA TTA GGT TTG GGG GAT AGG	1104
	Leu Ala Val Met Ser Met Val Gly Tyr Ile Leu Gly Leu Gly Asp Arg	
	355 360 365	
60	CAC CCA TCA AAT TTG ATG TTG GAC CGT ATT ACT GGG AAA GTC ATC CAT	1152
	His Pro Ser Asn Leu Met Leu Asp Arg Ile Thr Gly Lys Val Ile His	
	370 375 380	
65	ATT GAT TTC GGA GAC TGT TTT GAA GCA GCA ATA TTA CGT GAG AAG TAT	1200
	Ile Asp Phe Gly Asp Cys Phe Glu Ala Ala Ile Leu Arg Glu Lys Tyr	
	385 390 395 400	
70	CCA GAG AGA GTT CCG TTT AGA TTG ACG AGA ATG CTT AAT TAT GCC ATG	1248

	Pro Glu Arg Val Pro Phe Arg Leu Thr Arg Met Leu Asn Tyr Ala Met	
	405 410 415	
5	GAA GTT AGT GGA ATA GAG GGC TCG TTC AGA ATC ACA TGT GAA CAT GTT Glu Val Ser Gly Ile Glu Gly Ser Phe Arg Ile Thr Cys Glu His Val	1296
	420 425 430	
10	ATG AGG GTG TTG CGT GAT AAT AAA GAG TCT TTA ATG GCA ATA TTA GAG Met Arg Val Leu Arg Asp Asn Lys Glu Ser Leu Met Ala Ile Leu Glu	1344
	435 440 445	
15	GCC TTT GCT TAC GAT CCC TTG ATA AAT TGG GGG TTT GAT TTC CCA ACA Ala Phe Ala Tyr Asp Pro Leu Ile Asn Trp Gly Phe Asp Phe Pro Thr	1392
	450 455 460	
20	AAG GCG TTG GCT GAA TCA ACG GGT ATA CGT GTT CCA CAA GTC AAC ACT Lys Ala Leu Ala Glu Ser Thr Gly Ile Arg Val Pro Gln Val Asn Thr	1440
	465 470 475 480	
25	GCA GAA TTA TTA CGC AGA GGA CAG ATT GAC GAA AAA GAA GCT GTA AGA Ala Glu Leu Leu Arg Arg Gly Gln Ile Asp Glu Lys Glu Ala Val Arg	1488
	485 490 495	
30	TTG CAA AAG CAA AAT GAA TTG GAA ATA AGA AAC GCT AGA GCT GCA TTA Leu Gln Lys Gln Asn Glu Leu Glu Ile Arg Asn Ala Arg Ala Ala Leu	1536
	500 505 510	
35	GTG TTG AAA CGT ATT ACC GAT AAG TTA ACT GGT AAC GAT ATC AAA CGG Val Leu Lys Arg Ile Thr Asp Lys Leu Thr Gly Asn Asp Ile Lys Arg	1584
	515 520 525	
40	TTG AGA GGA TTA GAT GTG CCT ACT CAA GTC GAT AAA TTG ATT CAA CAA Leu Arg Gly Leu Asp Val Pro Thr Gln Val Asp Lys Leu Ile Gln Gln	1632
	530 535 540	
45	GCC ACC AGT GTT GAG AAT TTG TGT CAG CAT TAC ATT GGT TGG TGT TCG Ala Thr Ser Val Glu Asn Leu Cys Gln His Tyr Ile Gly Trp Cys Ser	1680
	545 550 555 560	
50	TGT TGG TAGGTTGATT ATCGTCATGT GTCGATAAGT ATGGTATTGT GGTAACATATT Cys Trp	1736
55	TTATAAAGGG AAATATTAAA GAATTGTATA TTATTAAAAA AAAAAAAAAA AACTCGAG	1794

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 562 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Leu Val Tyr Pro Leu Thr Val Ala Ile Thr Ser Glu Ser Thr Ser Arg

	1	5	10	15
	Lys	Lys	Ala	Ala
		Gln	Ser	Ile
		Ile	Glu	Lys
		Met	Arg	Val
		His	Ser	Pro
		20	25	30
5	Ser	Leu	Val	Asp
		Gln	Ala	Glu
		Leu	Val	Ser
		Arg	Glu	Leu
		ile	Arg	Val
		35	40	45
10	Ala	Val	Leu	Trp
		His	Glu	Gln
		Trp	His	Asp
		Ala	Leu	Glu
		Asp	Ala	Ser
		50	55	60
	Arg	Phe	Phe	Phe
		Gly	Glu	His
		Asn	Thr	Glu
		Lys	Met	Phe
		Glu	Thr	Leu
		65	70	75
15	Glu	Pro	Leu	His
		Gln	Met	Leu
		Gln	Lys	Gly
		Pro	Glu	Thr
		Met	Arg	Glu
		85	90	95
	Gln	Ala	Phe	Ala
		Asn	Ala	Phe
		Gly	Arg	Glu
		Leu	Thr	Asp
		Ala	Tyr	Glu
		100	105	110
20	Trp	Val	Leu	Asn
		Phe	Arg	Arg
		Thr	Lys	Asp
		Ile	Thr	Asn
		Leu	Asn	Gln
		115	120	125
	Ala	Trp	Asp	Ile
		Tyr	Tyr	Asn
		Val	Phe	Arg
		Arg	Val	Ser
		Lys	Gln	Val
		130	135	140
25	Gln	Leu	Leu	Ala
		Ser	Leu	Glu
		Leu	Gln	Tyr
		Val	Ser	Pro
		Asp	Leu	Glu
		145	150	155
30	His	Ala	Gln	Asp
		Leu	Glu	Leu
		Ala	Val	Pro
		Gly	Thr	Tyr
		Gln	Ala	Gly
		165	170	175
	Lys	Pro	Val	Ile
		Arg	Ile	Ile
		Lys	Phe	Asp
		Pro	Thr	Phe
		Ser	Ile	Ile
		180	185	190
35	Ser	Ser	Lys	Gln
		Arg	Pro	Arg
		Lys	Leu	Ser
		Cys	Arg	Gly
		Ser	Asp	Gly
		195	200	205
	Lys	Asp	Tyr	Gln
		Tyr	Ala	Leu
		Lys	Gly	His
		Glu	Asp	Ile
		Arg	Gln	Asp
		210	215	220
40	Asn	Leu	Val	Met
		Gln	Leu	Phe
		Gly	Leu	Val
		Asn	Thr	Leu
		Leu	Val	Asn
		225	230	235
45	Asp	Pro	Val	Cys
		Phe	Lys	Arg
		His	Leu	Asp
		Ile	Gln	Gln
		Tyr	Pro	Ala
		245	250	255
	Ile	Pro	Leu	Ser
		Pro	Lys	Val
		Gly	Leu	Leu
		Gly	Trp	Val
		Pro	Asn	Ser
		260	265	270
50	Asp	Thr	Phe	His
		Val	Leu	Ile
		Lys	Gly	Tyr
		Arg	Glu	Ser
		Arg	Ser	Ile
		275	280	285
	Met	Leu	Asn	Ile
		Glu	His	Arg
		Leu	Leu	Leu
		Gln	Met	Ala
		Pro	Asp	Tyr
		290	295	300
55	Asp	Phe	Leu	Thr
		Leu	Leu	Gln
		Lys	Val	Glu
		Val	Phe	Thr
		Ser	Ala	Met
		305	310	315
				320

Asp Asn Cys Lys Gly Gln Asp Leu Tyr Lys Val Leu Trp Leu Lys Ser
325 330 335

5 Lys Ser Ser Glu Ala Trp Leu Asp Arg Arg Thr Thr Tyr Thr Arg Ser
340 345 350

Leu Ala Val Met Ser Met Val Gly Tyr Ile Leu Gly Leu Gly Asp Arg
355 360 365

10 His Pro Ser Asn Leu Met Leu Asp Arg Ile Thr Gly Lys Val Ile His
370 375 380

Ile Asp Phe Gly Asp Cys Phe Glu Ala Ala Ile Leu Arg Glu Lys Tyr
15 385 390 395 400

Pro Glu Arg Val Pro Phe Arg Leu Thr Arg Met Leu Asn Tyr Ala Met
405 410 415

20 Glu Val Ser Gly Ile Glu Gly Ser Phe Arg Ile Thr Cys Glu His Val
420 425 430

Met Arg Val Leu Arg Asp Asn Lys Glu Ser Leu Met Ala Ile Leu Glu
435 440 445

25 Ala Phe Ala Tyr Asp Pro Leu Ile Asn Trp Gly Phe Asp Phe Pro Thr
450 455 460

Lys Ala Leu Ala Glu Ser Thr Gly Ile Arg Val Pro Gln Val Asn Thr
30 465 470 475 480

Ala Glu Leu Leu Arg Arg Gly Gln Ile Asp Glu Lys Glu Ala Val Arg
485 490 495

35 Leu Gln Lys Gln Asn Glu Leu Glu Ile Arg Asn Ala Arg Ala Ala Leu
500 505 510

Val Leu Lys Arg Ile Thr Asp Lys Leu Thr Gly Asn Asp Ile Lys Arg
515 520 525

40 Leu Arg Gly Leu Asp Val Pro Thr Gln Val Asp Lys Leu Ile Gln Gln
530 535 540

Ala Thr Ser Val Glu Asn Leu Cys Gln His Tyr Ile Gly Trp Cys Ser
45 545 550 555 560

Cys Trp

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- 5 (A) NAME/KEY: CDS
(B) LOCATION: 1..399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

10 GTT AGT CAC GAG TTG ATC AGA GTA GCC GTT CTA TGG CAC GAA TTA TGG 48
Val Ser His Glu Leu Ile Arg Val Ala Val Leu Trp His Glu Leu Trp
1 5 10 15

15 TAT GAA GGA CTG GAA GAT GCG AGC CGC CAA TTT TTC GTT GAA CAT AAC 96
Tyr Glu Gly Leu Glu Asp Ala Ser Arg Gln Phe Phe Val Glu His Asn
20 25 30

20 ATA GAA AAA ATG TTT TCT ACT TTA GAA CCT TTA CAT AAA CAC TTA GGC 144
Ile Glu Lys Met Phe Ser Thr Leu Glu Pro Leu His Lys His Leu Gly
35 40 45

25 AAT GAG CCT CAA ACG TTA AGT GAG GTA TCG TTT CAG AAA TCA TTT GGT 192
Asn Glu Pro Gln Thr Leu Ser Glu Val Ser Phe Gln Lys Ser Phe Gly
50 55 60

30 AGA GAT TTG AAC GAT GCC TAC GAA TGG TTG AAT AAC TAC AAA AAG TCA 240
Arg Asp Leu Asn Asp Ala Tyr Glu Trp Leu Asn Asn Tyr Lys Lys Ser
65 70 75 80

35 AAA GAC ATC AAT AAT TTG AAC CAA GCT TGG GAT ATT TAT TAT AAC GTC 288
Lys Asp Ile Asn Asn Leu Asn Gln Ala Trp Asp Ile Tyr Tyr Asn Val
85 90 95

40 TTC AGA AAA ATA ACA CGT CAA ATA CCA CAG TTA CAA ACC TTA GAC TTA 336
Phe Arg Lys Ile Thr Arg Gln Ile Pro Gln Leu Gln Thr Leu Asp Leu
100 105 110

40 CAG CAT GTT TCT CCC CAG CTT CTG GCT ACT CAT GAT CTC GAA TTG GCT 384
Gln His Val Ser Pro Gln Leu Leu Ala Thr His Asp Leu Glu Leu Ala
115 120 125

45 GTT CCT GGG ACA TAT 399
Val Pro Gly Thr Tyr
130

(2) INFORMATION FOR SEQ ID NO:16:

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 133 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Val Ser His Glu Leu Ile Arg Val Ala Val Leu Trp His Glu Leu Trp
 1 5 10 15
 Tyr Glu Gly Leu Glu Asp Ala Ser Arg Gln Phe Phe Val Glu His Asn
 5 20 25 30
 Ile Glu Lys Met Phe Ser Thr Leu Glu Pro Leu His Lys His Leu Gly
 35 40 45
 Asn Glu Pro Gln Thr Leu Ser Glu Val Ser Phe Gln Lys Ser Phe Gly
 10 50 55 60
 Arg Asp Leu Asn Asp Ala Tyr Glu Trp Leu Asn Asn Tyr Lys Lys Ser
 65 70 75 80
 Lys Asp Ile Asn Asn Leu Asn Gln Ala Trp Asp Ile Tyr Tyr Asn Val
 85 90 95
 Phe Arg Lys Ile Thr Arg Gln Ile Pro Gln Leu Gln Thr Leu Asp Leu
 20 100 105 110
 Gln His Val Ser Pro Gln Leu Leu Ala Thr His Asp Leu Glu Leu Ala
 115 120 125
 Val Pro Gly Thr Tyr
 25 130

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTC AGC CAC GAA TTG ATA CGT ATG GCG GTG CTT TGG CAT GAG CAA TGG 48
 Val Ser His Glu Leu Ile Arg Met Ala Val Leu Trp His Glu Gln Trp
 1 5 10 15
 TAT GAG GGT CTG GAT GAC GCC AGT AGG CAG TTT TTT GGA GAA CAT AAT 96
 Tyr Glu Gly Leu Asp Asp Ala Ser Arg Gln Phe Phe Gly Glu His Asn
 20 25 30
 ACC GAA AAA ATG TTT GCT GCT TTA GAG CCT CTG TAC GAA ATG CTG AAG 144
 Thr Glu Lys Met Phe Ala Ala Leu Glu Pro Leu Tyr Glu Met Leu Lys
 35 40 45

AGA GGA CCG GAA ACT TTG AGG GAA ATA TCG TTC CAA AAT TCT TTT GGT 192
Arg Gly Pro Glu Thr Leu Arg Glu Ile Ser Phe Gln Asn Ser Phe Gly
50 55 60

5 AGG GAC TTG AAT GAC GCT TAC GAA TGG CTG ATG AAT TAC AAA AAA TCT 240
Arg Asp Leu Asn Asp Ala Tyr Glu Trp Leu Met Asn Tyr Lys Lys Ser
65 70 75 80

10 AAA GAT GTT AGT AAT TTA AAC CAA GCG TGG GAC ATT TAC TAT AAT GTT 288
Lys Asp Val Ser Asn Leu Asn Gln Ala Trp Asp Ile Tyr Tyr Asn Val
85 90 95

15 TTC AGG AAA ATT GGT AAA CAG TTG CCA CAA TTA CAA ACT CTT GAA CTA 336
Phe Arg Lys Ile Gly Lys Gln Leu Pro Gln Leu Gln Thr Leu Glu Leu
100 105 110

CAA CAT GTG TCG CCA AAA CTA CTA TCT GCG CAT GAT TTG GAA TTG GCT 384
Gln His Val Ser Pro Lys Leu Leu Ser Ala His Asp Leu Glu Leu Ala
115 120 125

20 GTC CCC GGG ACC CGT 399
Val Pro Gly Thr Arg
130

25

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 133 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Val Ser His Glu Leu Ile Arg Met Ala Val Leu Trp His Glu Gln Trp
1 5 10 15

40 Tyr Glu Gly Leu Asp Asp Ala Ser Arg Gln Phe Phe Gly Glu His Asn
20 25 30

Thr Glu Lys Met Phe Ala Ala Leu Glu Pro Leu Tyr Glu Met Leu Lys
35 40 45

45 Arg Gly Pro Glu Thr Leu Arg Glu Ile Ser Phe Gln Asn Ser Phe Gly
50 55 60

50 Arg Asp Leu Asn Asp Ala Tyr Glu Trp Leu Met Asn Tyr Lys Lys Ser
65 70 75 80

Lys Asp Val Ser Asn Leu Asn Gln Ala Trp Asp Ile Tyr Tyr Asn Val
85 90 95

55 Phe Arg Lys Ile Gly Lys Gln Leu Pro Gln Leu Gln Thr Leu Glu Leu
100 105 110

Gln His Val Ser Pro Lys Leu Leu Ser Ala His Asp Leu Glu Leu Ala

115

120

125

Val Pro Gly Thr Arg
130

5

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 531 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

20 TGACCCTCAC CCCTTCCACC TATCCCAAAA ACCTCACTGG GTCTGTGGAC AAACAACANA 60
AATNTTTTCC ANANAGGCC CAAATGAGNC CCANGGGTCT NTCTTCCATC AGACCCAGTG 120
25 ATTCTGCGAC TCACACNCTT CAATTCAAGA CCTGACCNCT AGTAGGGAGG TTTANTCAGA 180
TCGCTGGCAN CCTCGGCTGA NCAGATNCAN AGNGGGGNTC GCTGTTCACT GGNCCACCC 240
TCNCTGGCCT TCTTCANCAG GGGTCTGGGA TGTTTTCACT GGNCCNAANA CNCTGTTTAG 300
30 AGCCAGGGCT CAGNAAACAG AAAANCTNTC ATGGNGGTTC TGGACACAGG GNAGGTCTGG 360
NACATATTGG GGATTATGAN CAGNACCAAN ACNCCACTAA ATNCCCCAAG NANAAAGTGT 420
35 AACCATNTCT ANACNCCATN TTNTATCAGN ANAAATTTTN TTCCNATAAA TGACATCAGN 480
ANTTTNAACA TNAAAAAAAAA AAAAAAAAAA AAAANAAAAA AAAAAAAAAA A 531

(2) INFORMATION FOR SEQ ID NO:20:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
45 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

50

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 128
(D) OTHER INFORMATION: /label= XhoI

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GCGTATAACG CGTTTGAAT CACTACAGGG ATGTTTAATA CCACTACAAT GGATGATGTA 60
TATAACTATC TATTCGATGA TGAAGATACC CCACCAAACC CAAAAAAGA GATCTGGAAT 120
5 TCGGATCCTC GAGAGATCTA TGAATCGTAG ATACTGAAAA ACCCCGCAAG TTCACTTCAA 180
CTGTGCATCG TGCACCATCT CAATTTCTTT CATTTATACA TCGTTTTGCC T 231

10 (2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TGAAGATACC CCACCAAACC C 21

25

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

40 TGCACAGTTG AAGTGAAC 18

(2) INFORMATION FOR SEQ ID NO:23:

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 662 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- 55 (A) NAME/KEY: CDS
(B) LOCATION: 60..416

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

	ACCAAACCCA AAAAAAGAGA TCCTAGNAAC TAGTGGATCC CCCGGGCTGC AGGAATTCG	59
5	GTA CGA GTC GCC CTC AGC AGA CTC GCC CAG GAG AGG AAA GCA TGG AGG Val Arg Val Ala Leu Ser Arg Leu Ala Gln Glu Arg Lys Ala Trp Arg 1 5 10 15	107
10	AAA GAC CAC CCA TTT GGT TTC GTG GCT GTC CCA ACA AAA AAT CCC GAT Lys Asp His Pro Phe Gly Phe Val Ala Val Pro Thr Lys Asn Pro Asp 20 25 30	155
15	GGC ACG ATG AAC CTC ATG AAC TGG GAG TGC GCC ATT CCA GGA AAG AAA Gly Thr Met Asn Leu Met Asn Trp Glu Cys Ala Ile Pro Gly Lys Lys 35 40 45	203
20	GGG ACT CCG TGG GAA GGA GGC TTG TTT AAA CTA CGG ATG CTT TTC AAA Gly Thr Pro Trp Glu Gly Gly Leu Phe Lys Leu Arg Met Leu Phe Lys 50 55 60	251
25	GAT GAT TAT CCA TCT TCG CCA CCA AAA TGT AAA TTC GAA CCA CCA TTA Asp Asp Tyr Pro Ser Ser Pro Pro Lys Cys Lys Phe Glu Pro Pro Leu 65 70 75 80	299
30	TTT CAC CCG AAT GTG TAC CCT TCG GGG ACA GTG TGC CTG TCC ATC TTA Phe His Pro Asn Val Tyr Pro Ser Gly Thr Val Cys Leu Ser Ile Leu 85 90 95	347
35	GAG GAG GAC AAG GAC TGG AGG GCA GNC ATC ACA ATC AAA CAG GAT CCT Glu Glu Asp Lys Asp Trp Arg Ala Xaa Ile Thr Ile Lys Gln Asp Pro 100 105 110	395
40	ATT AGG AAT ACA GGA ACT TTC TAAATGAACC AAATATCCAA GACCAGNTCA Ile Arg Asn Thr Gly Thr Phe 115	446
45	AGCAGAGGGC TACANGATTT ACTGCCAAAA CAGAGTNGNG TACGAGAAAG GGTCCGAGCA	506
50	NAGCCAGAAG TTTGGGCCTC ATTAGCAGGG ACCTGGTGGA TCGTCAAAGG AGGTTTGGTT	566
55	GGGAAGACTT GTTCAANATT TNGGAANTTA AGTTGTCCNN NAACTNGCGG GGGGGGGNNN	626
	NNCNNNTTNC CANTTCCCTN CCCCCNGTTT TTNGNT	662

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Val Arg Val Ala Leu Ser Arg Leu Ala Gln Glu Arg Lys Ala Trp Arg
1 5 10 15

Lys Asp His Pro Phe Gly Phe Val Ala Val Pro Thr Lys Asn Pro Asp
20 25 30

5 Gly Thr Met Asn Leu Met Asn Trp Glu Cys Ala Ile Pro Gly Lys Lys
35 40 45

Gly Thr Pro Trp Glu Gly Gly Leu Phe Lys Leu Arg Met Leu Phe Lys
50 55 60

10 Asp Asp Tyr Pro Ser Ser Pro Pro Lys Cys Lys Phe Glu Pro Pro Leu
65 70 75 80

15 Phe His Pro Asn Val Tyr Pro Ser Gly Thr Val Cys Leu Ser Ile Leu
85 90 95

Glu Glu Asp Lys Asp Trp Arg Ala Xaa Ile Thr Ile Lys Gln Asp Pro
100 105 110

20 Ile Arg Asn Thr Gly Thr Phe
115

(2) INFORMATION FOR SEQ ID NO:25:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 207 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCCTCCCTCC TGCCGCTCCT CTCTAGAACC TTCTAGAACC TGGGCTGTGC TGCTTTTGAG 60
40 CCTCAGACCC CAGGGCAGCA TCTCGGTTCT GCGCCACTTC CTTTGTGTTT ANATGGCGTT 120
TTGTCTGTGT TGCTGTTTAG AGTAGATNAA CTGTTTANAT AAAAAAAAAA NAAAATTNAC 180
TNGAGGGGGC NTGNAGGCAT GCNNAAC 207

45